

SEQUENCE LISTING

<110> Funahashi, Shin-ichi
 Miyata, Shoji
 Nomura, Nobuo
 Nagase, Takahiro
 Ohara, Osamu

<120> NOVEL GENE ENCODING BRAIN-SPECIFIC MEMBRANE PROTEIN

<130> 06501-081001

<140> 09/831,846

<141> 2001-05-15

<150> PCT/JP99/06449

<151> 1999-11-18

<150> JP 10/331727

<151> 1998-11-20

<160> 7

<210> 1

<211> 3144

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (466)..(2832)

<400> 1

```

gacctggctcc ctctcgctga gacacacata cactcacaca tacacaaccc ggcaggctcg      60
tctgaacttg aagacacccc acattccaag atgcccgagg ttccctgggaa tgcctgggggt      120
tcttcgatcc ggaaaatcct accggcatcc tctaggggag ggattattat tattattttt      180
ctttaatctg gaagagaaga gaacaagttg tgcttttccc cccttcttct tgctaaacgc      240
catggatata actgaataag cggtcagggt ctttccccgc gtggacgtcc gaggccacca      300
tctgacctga ttgcgcggag ccgcgcggag gtttagctcg agtctgtctc gggcggggaa      360
ggatgcgtgg ccgagccggg gagcccgggc gccccgcgga gccggcctcg gtgccacca      420
gccgggggta gatgctgcct cgcccaggcg ctgagtgacc agacc atg gag acc ctg      477
                                     Met Glu Thr Leu
                                     1

```

```

ctt ggt ggc ctg cta gcg ttt ggc atg gcg ttt gcc gtg gtc gac gcc      525
Leu Gly Gly Leu Leu Ala Phe Gly Met Ala Phe Ala Val Val Asp Ala
   5                10                15                20

```

```

tgc ccc aag tac tgt gtc tgc cag aat ctg tct gag tca ctg ggg acc      573
Cys Pro Lys Tyr Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr
          25                30                35

```

```

ctg tgc ccc tcc aag ggg ctg ctc ttt gta ccc cct gat att gac cgg      621
Leu Cys Pro Ser Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg
          40                45                50

```

cgg aca gtg gag ctg cgc ctg ggc ggc aac ttc atc atc cac atc agc Arg Thr Val Glu Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser 55 60 65	669
cgc cag gac ttt gcc aac atg acg ggg ctg gtg gac ctg acc ctg tcc Arg Gln Asp Phe Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser 70 75 80	717
agg aac acc atc agc cac atc cag ccc ttt tcc ttt ctg gac ctc gag Arg Asn Thr Ile Ser His Ile Gln Pro Phe Ser Phe Leu Asp Leu Glu 85 90 95 100	765
agc ctc cgc tcc ctg cat ctt gac agc aat cgg ctg cca agc ctt ggg Ser Leu Arg Ser Leu His Leu Asp Ser Asn Arg Leu Pro Ser Leu Gly 105 110 115	813
gag gac acc ctc cgg ggc ctg gtc aac ctg cag cac ctt atc gtg aac Glu Asp Thr Leu Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn 120 125 130	861
aac aac cag ctg ggc ggc atc gca gat gag gct ttt gag gac ttc ctg Asn Asn Gln Leu Gly Gly Ile Ala Asp Glu Ala Phe Glu Asp Phe Leu 135 140 145	909
ctg aca ttg gag gat ctg gac ctc tcc tac aac aac ctc cat ggc ctg Leu Thr Leu Glu Asp Leu Asp Leu Ser Tyr Asn Asn Leu His Gly Leu 150 155 160	957
ccg tgg gac tcc gtg cga cgc atg gtc aac ctc cac cag ctg agc ctg Pro Trp Asp Ser Val Arg Arg Met Val Asn Leu His Gln Leu Ser Leu 165 170 175 180	1005
gac cac aac ctg ctg gat cac atc gcc gag ggc acc ttt gca gac ctg Asp His Asn Leu Leu Asp His Ile Ala Glu Gly Thr Phe Ala Asp Leu 185 190 195	1053
cag aaa ctg gcc cgc ctg gat ctc acc tcc aat cgg ctg cag aag ctg Gln Lys Leu Ala Arg Leu Asp Leu Thr Ser Asn Arg Leu Gln Lys Leu 200 205 210	1101
ccc cct gat ccc atc ttt gcc cgc tcc cag gct tcg gct ttg aca gcc Pro Pro Asp Pro Ile Phe Ala Arg Ser Gln Ala Ser Ala Leu Thr Ala 215 220 225	1149
aca ccc ttt gcc cca ccc ttg tcc ttt agt ttt ggg ggt aac cca ctt Thr Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly Gly Asn Pro Leu 230 235 240	1197
cac tgc aat tgt gag ctt ctc tgg ctg cgg agg ctc gag cgg gac gat His Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu Glu Arg Asp Asp 245 250 255 260	1245
gac ctg gaa acc tgt ggc tcc cca ggg ggc ctc aag ggt cgc tac ttc Asp Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys Gly Arg Tyr Phe 265 270 275	1293
tgg cat gtg cgt gag gag gag ttt gtg tgc gag ccg cct ctc atc acc	1341

Trp	His	Val	Arg	Glu	Glu	Glu	Phe	Val	Cys	Glu	Pro	Pro	Leu	Ile	Thr		
			280					285					290				
cag	cac	aca	cac	aag	ttg	ctg	gtt	ctg	gag	ggc	cag	gcg	gcc	aca	ctc	1389	
Gln	His	Thr	His	Lys	Leu	Leu	Val	Leu	Glu	Gly	Gln	Ala	Ala	Thr	Leu		
		295					300					305					
aag	tgc	aaa	gcc	att	ggg	gac	ccc	agc	ccc	ctt	atc	cac	tgg	gta	gcc	1437	
Lys	Cys	Lys	Ala	Ile	Gly	Asp	Pro	Ser	Pro	Leu	Ile	His	Trp	Val	Ala		
	310					315					320						
ccc	gat	gac	cgc	ctg	gta	ggg	aac	tcc	tca	agg	acc	gct	gtc	tat	gac	1485	
Pro	Asp	Asp	Arg	Leu	Val	Gly	Asn	Ser	Ser	Arg	Thr	Ala	Val	Tyr	Asp		
325					330					335					340		
aat	ggc	acc	ctg	gac	atc	ttc	atc	acc	aca	tct	cag	gac	agt	ggg	gcc	1533	
Asn	Gly	Thr	Leu	Asp	Ile	Phe	Ile	Thr	Thr	Ser	Gln	Asp	Ser	Gly	Ala		
			345					350						355			
ttc	acc	tgc	att	gct	gcc	aat	gct	gcc	gga	gag	gcc	acg	gcc	atg	gtg	1581	
Phe	Thr	Cys	Ile	Ala	Ala	Asn	Ala	Ala	Gly	Glu	Ala	Thr	Ala	Met	Val		
			360				365					370					
gag	gtc	tcc	atc	gtc	cag	ctg	cca	cac	ctc	agc	aac	agc	acc	agc	cgc	1629	
Glu	Val	Ser	Ile	Val	Gln	Leu	Pro	His	Leu	Ser	Asn	Ser	Thr	Ser	Arg		
		375				380					385						
act	gca	ccc	ccc	aag	tcc	cgc	ctc	tca	gac	atc	act	ggc	tcc	agc	aag	1677	
Thr	Ala	Pro	Pro	Lys	Ser	Arg	Leu	Ser	Asp	Ile	Thr	Gly	Ser	Ser	Lys		
	390					395					400						
acc	agc	cgg	gga	ggg	gga	ggc	agt	ggg	ggc	gga	gag	cct	ccc	aaa	agc	1725	
Thr	Ser	Arg	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Glu	Pro	Pro	Lys	Ser		
405					410					415					420		
ccc	ccg	gaa	cgg	gct	gtg	ctt	gtg	tct	gaa	gtg	acc	acc	acc	tcg	gcc	1773	
Pro	Pro	Glu	Arg	Ala	Val	Leu	Val	Ser	Glu	Val	Thr	Thr	Thr	Ser	Ala		
				425				430						435			
ctg	gtc	aag	tgg	tct	gtc	agc	aag	tca	gca	ccc	cgg	gtg	aag	atg	tac	1821	
Leu	Val	Lys	Trp	Ser	Val	Ser	Lys	Ser	Ala	Pro	Arg	Val	Lys	Met	Tyr		
		440					445					450					
cag	ctg	cag	tac	aac	tgc	tct	gac	gat	gag	gta	ctg	att	tac	agg	atg	1869	
Gln	Leu	Gln	Tyr	Asn	Cys	Ser	Asp	Asp	Glu	Val	Leu	Ile	Tyr	Arg	Met		
		455					460					465					
atc	cca	gcc	tcc	aac	aag	gcc	ttc	gtg	gtc	aac	aac	ctg	gtg	tca	ggg	1917	
Ile	Pro	Ala	Ser	Asn	Lys	Ala	Phe	Val	Val	Asn	Asn	Leu	Val	Ser	Gly		
	470					475					480						
act	ggc	tac	gac	ttg	tgt	gtg	ctg	gcc	atg	tgg	gat	gac	aca	gcc	acg	1965	
Thr	Gly	Tyr	Asp	Leu	Cys	Val	Leu	Ala	Met	Trp	Asp	Asp	Thr	Ala	Thr		
485					490					495					500		
aca	ctc	acg	gcc	acc	aac	atc	gtg	ggc	tgc	gcc	cag	ttc	ttc	acc	aag	2013	
Thr	Leu	Thr	Ala	Thr	Asn	Ile	Val	Gly	Cys	Ala	Gln	Phe	Phe	Thr	Lys		

505										510					515					
gct	gac	tac	ccg	cag	tgc	cag	tcc	atg	cac	agc	cag	att	ctg	ggc	ggc					2061
Ala	Asp	Tyr	Pro	Gln	Cys	Gln	Ser	Met	His	Ser	Gln	Ile	Leu	Gly	Gly					
			520					525					530							
acc	atg	atc	ctg	gtc	atc	ggg	ggc	atc	atc	gtg	gcc	acg	ctg	ctg	gtc					2109
Thr	Met	Ile	Leu	Val	Ile	Gly	Gly	Ile	Ile	Val	Ala	Thr	Leu	Leu	Val					
		535					540					545								
ttc	atc	gtc	atc	ctc	atg	gtg	cgc	tac	aag	gtc	tgc	aac	cac	gag	gcc					2157
Phe	Ile	Val	Ile	Leu	Met	Val	Arg	Tyr	Lys	Val	Cys	Asn	His	Glu	Ala					
	550					555					560									
ccc	agc	aag	atg	gca	gcg	gcc	gtg	agc	aat	gtg	tac	tcg	cag	acc	aac					2205
Pro	Ser	Lys	Met	Ala	Ala	Ala	Val	Ser	Asn	Val	Tyr	Ser	Gln	Thr	Asn					
565					570				575						580					
ggc	gcc	cag	cca	ccg	cct	cca	agc	agc	gca	cca	gcc	ggg	gcc	ccg	ccg					2253
Gly	Ala	Gln	Pro	Pro	Pro	Pro	Ser	Ser	Ala	Pro	Ala	Gly	Ala	Pro	Pro					
			585						590					595						
cag	ggc	ccg	ccg	aag	gtg	gtg	gtg	cgc	aac	gag	ctc	ctg	gac	ttc	acc					2301
Gln	Gly	Pro	Pro	Lys	Val	Val	Val	Arg	Asn	Glu	Leu	Leu	Asp	Phe	Thr					
			600					605					610							
gcc	agc	ctg	gcc	cgc	gcc	agt	gac	tcc	tct	tcc	tcc	agc	tcc	ctg	ggc					2349
Ala	Ser	Leu	Ala	Arg	Ala	Ser	Asp	Ser	Ser	Ser	Ser	Ser	Ser	Leu	Gly					
		615					620					625								
agt	ggg	gag	gct	gcg	ggg	ctg	gga	cgg	gcc	ccc	tgg	agg	atc	cca	ccc					2397
Ser	Gly	Glu	Ala	Ala	Gly	Leu	Gly	Arg	Ala	Pro	Trp	Arg	Ile	Pro	Pro					
	630					635					640									
tcc	gcc	ccg	cgc	ccc	aag	ccc	agc	ctt	gac	cgc	ctg	atg	ggg	gcc	ttc					2445
Ser	Ala	Pro	Arg	Pro	Lys	Pro	Ser	Leu	Asp	Arg	Leu	Met	Gly	Ala	Phe					
645					650				655						660					
gcc	tcc	ctg	gac	ctc	aag	agt	cag	aga	aag	gag	gag	ctg	ctg	gac	tcc					2493
Ala	Ser	Leu	Asp	Leu	Lys	Ser	Gln	Arg	Lys	Glu	Glu	Leu	Leu	Asp	Ser					
			665						670					675						
agg	act	cca	gcc	ggg	aga	ggg	gct	ggg	acg	tcg	gcc	cgg	ggc	cac	cac					2541
Arg	Thr	Pro	Ala	Gly	Arg	Gly	Ala	Gly	Thr	Ser	Ala	Arg	Gly	His	His					
		680						685				690								
tcg	gac	cga	gag	cca	ctg	ctg	ggg	ccc	cct	gcg	gcc	cgg	gcc	agg	agc					2589
Ser	Asp	Arg	Glu	Pro	Leu	Leu	Gly	Pro	Pro	Ala	Ala	Arg	Ala	Arg	Ser					
		695					700					705								
ctg	ctc	ccc	ttg	ccg	ttg	gag	ggc	aag	gcc	aaa	cgc	agc	cac	tcc	ttc					2637
Leu	Leu	Pro	Leu	Pro	Leu	Glu	Gly	Lys	Ala	Lys	Arg	Ser	His	Ser	Phe					
	710					715					720									
gac	atg	ggg	gac	ttt	gct	gct	gcg	gcg	gcg	gga	ggg	gtc	gtg	ccg	ggc					2685
Asp	Met	Gly	Asp	Phe	Ala	Ala	Ala	Ala	Ala	Gly	Gly	Val	Val	Pro	Gly					
725					730					735					740					

2061
2109
2157
2205
2253
2301
2349
2397
2445
2493
2541
2589
2637
2685

ggc tac agt cct cct cgg aag gtc tcg aac atc tgg acg aag cgc agc 2733
 Gly Tyr Ser Pro Pro Arg Lys Val Ser Asn Ile Trp Thr Lys Arg Ser
 745 750 755

ctc tct gtc aac ggc atg ctc ttg ccc ttt gag gag agt gac ctg gtg 2781
 Leu Ser Val Asn Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu Val
 760 765 770

ggg gcc cgg ggg act ttt ggc agc tcc gaa tgg gtg atg gag agc acg 2829
 Gly Ala Arg Gly Thr Phe Gly Ser Ser Glu Trp Val Met Glu Ser Thr
 775 780 785

gtc taggtggggg tgggcatgct ccttttctg tgcgcagggt gggagaaggg 2882
 Val

gaaagaatct cactggcaag tgtttggtga gtttccatgg tgatgtttac atccagggac 2942
 agtttcgtct cctgtgcaat ggcctcgtgt cccccctac cccgcaacac ccacatcacc 3002
 tccccaccac ccggccgggg tgtgctcagg gaatgtggac tcgctcaaata gccggactga 3062
 gccctgagtg tttggaaagg cgagactccg cctttctaata cacaaatgta gcctacaagc 3122
 aagcggtctt ggattgctta tg 3144

<210> 2

<211> 789

<212> PRT

<213> Homo sapiens

<400> 2

Met	Glu	Thr	Leu	Leu	Gly	Gly	Leu	Leu	Ala	Phe	Gly	Met	Ala	Phe	Ala
1				5					10					15	
Val	Val	Asp	Ala	Cys	Pro	Lys	Tyr	Cys	Val	Cys	Gln	Asn	Leu	Ser	Glu
			20					25				30			
Ser	Leu	Gly	Thr	Leu	Cys	Pro	Ser	Lys	Gly	Leu	Leu	Phe	Val	Pro	Pro
		35					40					45			
Asp	Ile	Asp	Arg	Arg	Thr	Val	Glu	Leu	Arg	Leu	Gly	Gly	Asn	Phe	Ile
	50				55					60					
Ile	His	Ile	Ser	Arg	Gln	Asp	Phe	Ala	Asn	Met	Thr	Gly	Leu	Val	Asp
65				70					75					80	
Leu	Thr	Leu	Ser	Arg	Asn	Thr	Ile	Ser	His	Ile	Gln	Pro	Phe	Ser	Phe
			85					90					95		
Leu	Asp	Leu	Glu	Ser	Leu	Arg	Ser	Leu	His	Leu	Asp	Ser	Asn	Arg	Leu
		100						105					110		
Pro	Ser	Leu	Gly	Glu	Asp	Thr	Leu	Arg	Gly	Leu	Val	Asn	Leu	Gln	His
		115					120					125			
Leu	Ile	Val	Asn	Asn	Asn	Gln	Leu	Gly	Gly	Ile	Ala	Asp	Glu	Ala	Phe
	130					135					140				
Glu	Asp	Phe	Leu	Leu	Thr	Leu	Glu	Asp	Leu	Asp	Leu	Ser	Tyr	Asn	Asn
145				150					155					160	
Leu	His	Gly	Leu	Pro	Trp	Asp	Ser	Val	Arg	Arg	Met	Val	Asn	Leu	His
			165				170						175		
Gln	Leu	Ser	Leu	Asp	His	Asn	Leu	Leu	Asp	His	Ile	Ala	Glu	Gly	Thr
		180					185					190			
Phe	Ala	Asp	Leu	Gln	Lys	Leu	Ala	Arg	Leu	Asp	Leu	Thr	Ser	Asn	Arg
		195				200					205				
Leu	Gln	Lys	Leu	Pro	Pro	Asp	Pro	Ile	Phe	Ala	Arg	Ser	Gln	Ala	Ser
	210					215					220				

Ala Leu Thr Ala Thr Pro Phe Ala Pro Pro Leu Ser Phe Ser Phe Gly
 225 230 235 240
 Gly Asn Pro Leu His Cys Asn Cys Glu Leu Leu Trp Leu Arg Arg Leu
 245 250 255
 Glu Arg Asp Asp Asp Leu Glu Thr Cys Gly Ser Pro Gly Gly Leu Lys
 260 265 270
 Gly Arg Tyr Phe Trp His Val Arg Glu Glu Glu Phe Val Cys Glu Pro
 275 280 285
 Pro Leu Ile Thr Gln His Thr His Lys Leu Leu Val Leu Glu Gly Gln
 290 295 300
 Ala Ala Thr Leu Lys Cys Lys Ala Ile Gly Asp Pro Ser Pro Leu Ile
 305 310 315 320
 His Trp Val Ala Pro Asp Asp Arg Leu Val Gly Asn Ser Ser Arg Thr
 325 330 335
 Ala Val Tyr Asp Asn Gly Thr Leu Asp Ile Phe Ile Thr Thr Ser Gln
 340 345 350
 Asp Ser Gly Ala Phe Thr Cys Ile Ala Ala Asn Ala Ala Gly Glu Ala
 355 360 365
 Thr Ala Met Val Glu Val Ser Ile Val Gln Leu Pro His Leu Ser Asn
 370 375 380
 Ser Thr Ser Arg Thr Ala Pro Pro Lys Ser Arg Leu Ser Asp Ile Thr
 385 390 395 400
 Gly Ser Ser Lys Thr Ser Arg Gly Gly Gly Gly Ser Gly Gly Gly Glu
 405 410 415
 Pro Pro Lys Ser Pro Pro Glu Arg Ala Val Leu Val Ser Glu Val Thr
 420 425 430
 Thr Thr Ser Ala Leu Val Lys Trp Ser Val Ser Lys Ser Ala Pro Arg
 435 440 445
 Val Lys Met Tyr Gln Leu Gln Tyr Asn Cys Ser Asp Asp Glu Val Leu
 450 455 460
 Ile Tyr Arg Met Ile Pro Ala Ser Asn Lys Ala Phe Val Val Asn Asn
 465 470 475 480
 Leu Val Ser Gly Thr Gly Tyr Asp Leu Cys Val Leu Ala Met Trp Asp
 485 490 495
 Asp Thr Ala Thr Thr Leu Thr Ala Thr Asn Ile Val Gly Cys Ala Gln
 500 505 510
 Phe Phe Thr Lys Ala Asp Tyr Pro Gln Cys Gln Ser Met His Ser Gln
 515 520 525
 Ile Leu Gly Gly Thr Met Ile Leu Val Ile Gly Gly Ile Ile Val Ala
 530 535 540
 Thr Leu Leu Val Phe Ile Val Ile Leu Met Val Arg Tyr Lys Val Cys
 545 550 555 560
 Asn His Glu Ala Pro Ser Lys Met Ala Ala Val Ser Asn Val Tyr
 565 570 575
 Ser Gln Thr Asn Gly Ala Gln Pro Pro Pro Ser Ser Ala Pro Ala
 580 585 590
 Gly Ala Pro Pro Gln Gly Pro Pro Lys Val Val Val Arg Asn Glu Leu
 595 600 605
 Leu Asp Phe Thr Ala Ser Leu Ala Arg Ala Ser Asp Ser Ser Ser
 610 615 620
 Ser Ser Leu Gly Ser Gly Glu Ala Ala Gly Leu Gly Arg Ala Pro Trp
 625 630 635 640
 Arg Ile Pro Pro Ser Ala Pro Arg Pro Lys Pro Ser Leu Asp Arg Leu
 645 650 655
 Met Gly Ala Phe Ala Ser Leu Asp Leu Lys Ser Gln Arg Lys Glu Glu
 660 665 670
 Leu Leu Asp Ser Arg Thr Pro Ala Gly Arg Gly Ala Gly Thr Ser Ala

```
<210> 3
<211> 44
<212> DNA
<213> Artificial Sequence
```

<400> 3
gactagttct agatcgcgaq cggccgccct tttttttttt tttt 44

<220>
<223> Description of Artificial Sequence: an artificially synthesized adapter sequence.

<400> 4
tcgacccacg cgtccg 16

<220>
<223> Description of Artificial Sequence: an artificially synthesized adapter sequence.

<400> 5
cggacgcgtg gg 12

```
<210> 6
<211> 25
<212> DNA
<213> Artificial Sequence
```

<220>

<223> Description of Artificial Sequence: an
artificially synthesized primer sequence.

<400> 6

caggggtggga gaaggggaaa gaatc

25

<210> 7

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: an
artificially synthesized primer sequence.

<400> 7

gaggccattg acagggagac gaaac

25

gaggccattg acagggagac gaaac